

5' GCC AGC TGC GTT CTG AGC CTG GGC GCA GCT ACC ATC TGC TCT GGG AAG CAC CAG

11 20 29 38 47 56

GGT GTC CCC GCC GCC CTC AGC TCG AAG TCA GCC ACC ATG GAG GCG CAG GCA CAA

65 74 83 92 101 110

M E A Q A Q

GGT TTG TTG GAG ACT GAA CCG TTG CAA GGA ACA GAC GAA GAT GCA GTA GCC AGT

119 128 137 146 155 164

G L L E T E P L Q G T D E D A V A S

GCT GAC TTC TCT AGC ATG CTC TCT GAG GAG GAA AAG GAA GAG TTA AAA GCA GAG

173 182 191 200 209 218

A D F S S M L S E E E K E E L K A E

TTA GTT CAG CTA GAA GAC GAA ATT ACA ACA CTA CGA CAA GTT TTG TCA GCG AAA

227 236 245 254 263 272

L V Q L E D E I T T L R Q V L S A K

GAA AGG CAT CTA GTT GAG ATA AAA CAA AAA CTC GGC ATG AAC CTG ATG AAT GAA

281 290 299 308 317 326

E R H L V E I K Q K L G M N L M N E

TTA AAA CAG AAC TTC AGC AAA AGC TGG CAT GAC ATG CAG ACT ACC ACT GCC TAC

335 344 353 362 371 380

L K Q N F S K S W H D M Q T T T A Y

AAG AAA ACA CAT GAA ACC CTG AGT CAC GCA GGG CAA AAG GCA ACT GCA GCT TTC

389 398 407 416 425 434

K K T H E T L S H A G Q K A T A A F

AGC AAC GTT GGA ACG GCC ATC AGC AAG AAG TTC GGA GAC ATG AGT TAC TCC ATT

443 452 461 470 479 488

S N V G T A I S K K F G D M S Y S I

CGC CAT TCC ATA AGT ATG CCT GCT ATG AGG AAT TCT CCT ACT TTC AAA TCA TTT

497 506 515 524 533 542

R H S I S M P A M R N S P T F K S F

GAG GAG AGG GTT GAG ACA ACT GTC ACA AGC CTC AAG ACG AAA GTA GGC GGT ACG

551 560 569 578 587 596

E E R V E T T V T S L K T K V G G T

AAC CCT AAT GGA GGC AGT TTT GAG GAG GTC CTC AGC TCC ACG GCC CAT GCC AGT

605 614 623 632 641 650

N P N G G S F E E V L S S T A H A S

GCC CAG AGC TTG GCA GGA GGC TCC CGG CGG ACC AAG GAG GAG GAG CTG CAG TGC

659 668 677 686 695 704

A Q S L A G G S R R T K E E E L Q C

09162597.092999

FIGURE 1A

365260" 26529760

		713			722			731			740			749			758
TAA	GTC	CAG	CCA	GCG	TGC	AGT	GCA	TCC	AGA	AAC	CGG	CCA	CTA	CCC	AGC	CCA	TCT
		767			776			785									
NTG	CCT	GTG	CTT	ATC	CAG	ATA	AGA	AGA	CCA	AA	3'						

FIGURE 1B

5'	TMG	MKC	10	GCG	GGC	CCC	19	CGC	CAG	TCA	28	GGT	GGG	TGC	37	CAG	GCC	CTG	46	GCC	GTG	GCG	55	AAA		
			64	GAG	CCG	GCG	GAG	GGA	73	GGA	CCC	GCT	CCC	GGA	GAC	91	GCC	GCC	TCG	100	CGA	TCC	CCG	109	CGC	
			118	GGG	CGG	GAC	CGG	GCG	127	GCC	GGC	ATC	136	ATG	ACC	CTG	145	TTT	CAC	154	GGG	AAC	TGC	163	TTC	
													M	T	L	F	H	F	G	N	C	F				
			172	GCT	CTT	GCC	TAC	TTC	181	CCC	TAC	TTC	190	ATC	ACC	TAC	199	AAG	TGC	208	AGC	GGC	CTG	217	TCC	
			A	L	A	Y	F	P	Y	F	I	T	Y	K	C	S	G	L	S	E						
			226	TAC	AAC	GCC	TTC	TGG	235	AAA	TGC	GTC	244	CAG	GCT	GGA	253	GTC	ACC	262	TAC	CTC	TTT	GTC	271	CAA
			Y	N	A	F	W	K	C	V	Q	A	G	V	T	Y	L	F	V	Q						
			280	CTC	TGC	AAG	ATG	CTG	289	TTC	TTG	GCC	298	ACT	TTC	TTT	307	CCC	ACC	316	TGG	GAA	GGC	GGC	325	ATC
			L	C	K	M	L	F	L	A	T	F	F	P	T	W	E	G	G	I						
			334	TAT	GAC	TTC	ATT	GGG	343	GAG	TTC	ATG	352	AAG	GCC	AGC	361	GTG	GAT	370	GTG	GCA	GAC	CTG	379	ATA
			Y	D	F	I	G	E	F	M	K	A	S	V	D	V	A	D	L	I						
			388	GGT	CTA	AAC	CTT	GTC	397	ATG	TCC	CGG	406	AAT	GCC	GGC	415	AAG	GGA	424	GAG	TAC	AAG	ATC	433	ATG
			G	L	N	L	V	M	S	R	N	A	G	K	G	E	Y	K	I	M						
			442	GTT	GCT	GCC	CTG	GGC	451	TGG	GCC	ACT	460	GCT	GAG	CTT	469	ATT	ATG	478	TCC	CGC	TGC	ATT	487	CCC
			V	A	A	L	G	W	A	T	A	E	L	I	M	S	R	C	I	P						
			496	CTA	TGG	GTC	GGA	GCC	505	CGG	GGC	ATT	514	GAG	TTT	GAC	523	TGG	AAG	532	TAC	ATC	CAG	ATG	541	AGC
			L	W	V	G	A	R	G	I	E	F	D	W	K	Y	I	Q	M	S						
			550	ATA	GAC	TCC	AAC	ATC	559	AGT	CTG	GTC	568	CAT	TAC	ATC	577	GTC	GCG	586	TCT	GCT	CAG	GTC	595	TGG
			I	D	S	N	I	S	L	V	H	Y	I	V	A	S	A	Q	V	W						
			604	ATG	ATA	ACA	CGC	TAT	613	GAT	CTG	TAC	622	CAC	AAC	TTC	631	CGG	CCA	640	GCT	GTC	CTT	CTG	649	CTG
			M	I	T	R	Y	D	L	Y	H	N	F	R	P	A	V	L	L	L						
			658	ATG	TTC	CTC	AGT	GTC	667	TAC	AAG	GCC	676	TTT	GTT	ATG	685	GAG	ACC	694	TTC	GTC	CAC	CTC	703	TGC
			M	F	L	S	V	Y	K	A	F	V	M	E	T	F	V	H	L	C						
			712	TCG	CTG	GGC	AGT	TGG	721	GCA	RCT	CTA	730	MTG	GCC	CGA	739	GCA	GTG	748	GTA	ACG	GGG	CTG	757	CTG
			S	L	G	S	W	A	X	L	X	A	R	A	V	V	T	G	L	L						

FIGURE 2A

		766			775			784			793			802		811
GCC	CTC	AAG	CAC	TTT	GGG	CCT	GTA	TGT	CGS	CGT	TGT	CAA	TGT	GCA	CTY	CTA
A	L	K	H	F	G	P	V	C	R	R	C	Q	C	A	L	L
																G
		820			829			838			847			856		865
TTG	GTG	TCT	CAG	ACA	TTG	ATG	TAC	CTT	TTC	CCT	GCC	TCA	CTC	CAG	GTT	TTA
L	V	S	Q	T	L	M	Y	L	F	P	A	S	L	Q	V	L
																V
		874			883											
AAG	TAA	ACA	GTA	TTT	GGA	AAG	TT	3'								
K																

FIGURE 2B

09162597-099260-46529760

Library	Lib Description	Abun	Pct	Abun
BRAINOM02	brain, 55 M, NORM, WM	1	0.0454	
UTRSNOT01	uterus, 59 F	1	0.0393	
TYMNOR01	lymphocytes (non-adher PBMNC), 24 M, RP	1	0.0372	
BRSTNOT02	breast, 55 F, match to BRSTTUT01	2	0.0317	
PROSTUT08	prostate tumor, 60 M, match to PROSNOT14	1	0.0266	
PROSNOT14	prostate, 60 M, match to PROSTUT08	1	0.0256	
LIVRNOM01	liver, 49 M, WM	1	0.0254	
PROSNOT15	prostate, 66 M, match to PROSTUT10	1	0.0241	
NERVMSM01	multiple sclerosis, 46 M, NORM, WM	1	0.0228	
HNT2AGT01	hNT2 cell line, post-mitotic neurons	1	0.0190	
BRAITUT02	brain tumor, metastasis, 58 M	1	0.0169	
LIVSFEM02	liver/spleen, fetal M, NORM, WM	2	0.0053	

Electronic Northern Results returned a total of 12 row(s).

FIGURE 3

Library	Lib Description	Abun	Pct	Abun
COLNNOT22	colon, 56 F	2	0.0554	
COLNPOT01	colon polyp, 40 F	2	0.0513	
PROSNOT18	prostate, hyperplasia, 58 M	2	0.0513	
MUSCNOT02	muscle, psoas, 12 M	1	0.0382	
STOMTUT01	stomach tumor, 52 M, match to STOMNOT02	1	0.0368	
SINTNOT02	small intestine, 55 F	1	0.0345	
LVENNOT03	heart, left ventricle, 31 M	1	0.0337	
MMLR3DT01	macrophages (adher PBMNC), M/F, 72-hr MLR	1	0.0331	
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	1	0.0310	
LUNGTUT03	lung tumor, 69 M, match to LUNGNOT15	1	0.0308	
BLADTUT02	bladder tumor, 80 F, match to BLADNOT03	1	0.0305	
BRAITUT08	brain tumor, astrocytoma, 47 M	2	0.0293	
PROSTUT12	prostate tumor, 65 M, match to PROSNOT20	1	0.0279	
BLADNOT04	bladder, 28 M	1	0.0278	
TESTTUT02	testicular tumor, 31 M	1	0.0278	
THYRNOT03	thyroid tumor, adenoma, 28 F	2	0.0277	
SINTNOT13	small intestine, ileum, ulcerative cholangitis, 25 F	1	0.0275	
COLNTUT03	colon tumor, 62 M, match to COLNNOT16	1	0.0272	
BLADTUT05	bladder tumor, 66 M, match to BLADNOT06	1	0.0268	
KIDNTUT01	kidney tumor, Wilms, 8m F	1	0.0267	
PENITUT01	penis tumor, carcinoma, 64 M	1	0.0267	
COLNNOT23	colon, 16 M	1	0.0264	
BRAITUT13	brain tumor, meningioma, 68 M	1	0.0262	
LIVRTUT01	liver tumor, metastasis, 51 F	1	0.0259	
PROSNOT14	prostate, 60 M, match to PROSTUT08	1	0.0256	
BRSTTUT08	breast tumor, 45 F, match to BRSTNOT09	1	0.0254	
BMARNOT03	bone marrow, 16 M	1	0.0242	
RATRNOT02	heart, right atrium, 39 M	1	0.0236	
PANCNOT01	pancreas, 29 M	1	0.0214	
LUNGNOT04	lung, 2 M	1	0.0183	
SYNORAT04	synovium, wrist, rheumatoid, 62 F	1	0.0174	
PLACNOT02	placenta, fetal F	1	0.0168	
BRSTNOT03	breast, 54 F, match to BRSTTUT02	1	0.0147	
SPLNNOT04	spleen, 2 M	1	0.0128	
PROSNOT06	prostate, 57 M, match to PROSTUT04	1	0.0114	
LUNGFET03	lung, fetal F	1	0.0091	

Electronic Northern Results returned a total of 36 row(s).

FIGURE 4

1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	E	A	Q	A	Q		SEQ ID NO-1									
1	M	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	D	R	G	E	O		SEQ ID NO-5									
1	M	P	K	G	N	K	K	P	N	E	K	K	E	E	L	E	K	F	A	K	E	L	Q	G	S	D	S	D	E	D		SEQ ID NO-6	
7	G	L	L	E	T	E	P	L	Q	G	T	D	-	E	D	A	V	A	S	A	D	F	S	S	M	L	S	E	E	E	E		SEQ ID NO-1
7	G	L	L	R	T	D	P	V	P	E	E	G	-	E	D	V	A	A	T	I	S	A	T	E	T	L	S	E	E	E	E		SEQ ID NO-5
31	A	V	V	I	E	Q	P	T	V	E	P	K	L	P	Q	N	D	S	S	S	S	N	K	I	V	L	S	Q	A	E		SEQ ID NO-6	
36	K	E	E	L	K	A	E	L	V	Q	L	E	D	E	I	T	T	L	R	Q	V	L	S	A	K	E	R	H	L	V		SEQ ID NO-1	
36	Q	E	E	L	R	R	E	L	A	K	V	E	E	E	I	Q	T	L	S	Q	V	L	A	A	K	E	K	H	L	A		SEQ ID NO-5	
61	K	D	L	L	R	T	E	L	D	K	T	E	E	E	I	S	T	L	K	Q	V	L	S	A	R	Q	K	H	A	A		SEQ ID NO-6	
66	E	I	K	Q	K	L	G	M	N	L	M	N	E	L	K	Q	N	F	S	K	S	W	H	D	M	Q	T	T	T	A		SEQ ID NO-1	
66	E	I	K	R	K	L	G	I	N	S	L	Q	E	L	K	Q	N	I	A	K	G	W	Q	D	V	T	A	T	S	A		SEQ ID NO-5	
91	E	L	K	R	K	L	G	L	T	P	F	S	E	L	S	Q	D	I	N	R	S	L	K	T	V	T	D	T	D	A		SEQ ID NO-6	
96	Y	K	K	T	H	E	T	L	S	H	A	G	Q	K	A	T	A	A	F	-	-	-	-	S	N	V	G	T	A		SEQ ID NO-1		
96	Y	K	K	T	S	E	T	L	S	Q	A	G	Q	K	A	S	A	A	F	-	-	-	-	S	S	V	G	S	V		SEQ ID NO-5		
121	C	T	H	F	I	E	I	N	I	Q	K	K	K	K	Q	S	M	Y	Y	I	K	R	L	S	K	N	I	Q	T	V		SEQ ID NO-6	
121	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	S	K	K	F	G	D	M	S	-	-	-	-	-		SEQ ID NO-1	
121	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	I	T	K	K	L	E	D	-	-	-	-	-	-	-		SEQ ID NO-5	
151	P	I	L	T	S	E	K	K	R	I	L	H	A	F	I	V	L	K	K	K	S	S	I	L	K	S	L	L	L	L	W		SEQ ID NO-6
130	-	-	Y	S	I	R	H	S	I	S	M	P	A	-	-	-	-	-	-	-	-	-	-	M	R	N	S	P	T	F		SEQ ID NO-1	
128	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	V	K	N	S	P	T	F		SEQ ID NO-5		
181	Q	Q	Y	Q	K	T	A	E	V	A	A	A	T	S	D	T	V	K	E	K	W	N	D	M	R	N	S	S	L	F		SEQ ID NO-6	
148	K	S	F	E	E	R	V	E	T	T	V	T	S	L	K	T	K	V	G	G	T	N	P	N	G	G	S	F	E	E		SEQ ID NO-1	
135	K	S	F	E	E	K	V	E	-	-	-	-	N	L	K	S	K	V	G	G	T	K	P	A	G	G	D	F	G	E		SEQ ID NO-5	
211	K	S	F	E	S	K	L	G	S	A	L	N	N	-</																			

FIGURE 5

1	M	T	L	F	H	F	G	N	C	F	A	L	A	Y	F	P	Y	F	I	T	Y	K	C	S	G	L	S	E	Y	N	SEQ ID NO-3
1	M	S	F	F	H	F	I	N	C	F	A	L	A	F	A	P	Y	F	I	V	Y	K	Y	S	G	I	N	E	Y	S	SEQ ID NO-7
31	A	F	W	K	C	V	Q	A	G	V	T	Y	L	F	V	Q	L	C	K	M	L	F	L	A	T	F	F	P	T	W	SEQ ID NO-3
31	S	I	W	K	C	A	T	A	S	G	G	Y	L	L	T	Q	L	A	K	L	L	I	I	A	T	F	F	P	A	L	SEQ ID NO-7
61	E	G	G	I	Y	D	F	I	G	E	F	M	K	A	S	V	D	V	A	D	L	I	G	L	N	L	V	M	S	R	SEQ ID NO-3
61	D	S	E	G	F	S	I	V	P	E	F	L	K	S	S	A	D	I	I	D	V	I	G	L	H	L	L	M	T	N	SEQ ID NO-7
91	-	N	A	G	K	G	E	Y	K	I	M	V	A	A	L	G	W	A	T	A	E	L	I	M	S	R	C	I	P	L	SEQ ID NO-3
91	F	L	A	G	K	G	E	V	R	F	V	V	G	G	L	G	W	G	F	A	H	S	V	A	H	R	L	V	L	L	SEQ ID NO-7
120	W	V	G	A	R	G	I	E	F	D	W	K	Y	I	Q	M	S	I	D	S	N	I	S	L	V	H	Y	I	V	A	SEQ ID NO-3
121	W	V	G	A	R	G	T	A	F	T	W	R	W	V	O	T	S	L	D	S	S	A	D	L	L	V	I	V	S	L	SEQ ID NO-7
150	S	A	Q	V	W	M	I	T	R	Y	D	L	Y	H	N	F	R	P	A	V	L	L	L	M	F	L	S	V	Y	K	SEQ ID NO-3
151	A	C	L	T	W	M	I	T	R	-	-	-	-	-	-	-	T	P	N	K	F	L	V	S	-	-	P	I	L	A	SEQ ID NO-7
180	A	F	V	M	E	T	F	V	H	L	C	S	L	G	S	W	A	R	L	D	A	R	-	-	-	A	V	V	T	G	SEQ ID NO-3
172	I	T	V	O	H	T	F	-	-	-	-	S	L	Y	G	W	S	L	L	A	F	R	F	A	Y	S	I	A	T	A	SEQ ID NO-7
207	L	L	A	L	K	H	F	G	P	V	C	R	R	C	Q	C	A	L	L	G	L	V	S	O	T	L	M	Y	L	F	SEQ ID NO-3
198	I	L	T	V	V	V	Y	S	A	-	-	N	R	T	A	S	T	R	K	N	-	-	-	-	-	-	-	-	-	-	SEQ ID NO-7
237	P	A	S	L	O	V	L	V	K	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SEQ ID NO-3	
216	-	-	-	-	-	-	-	-	E	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	SEQ ID NO-7	

FIGURE 6

001539.0929T60

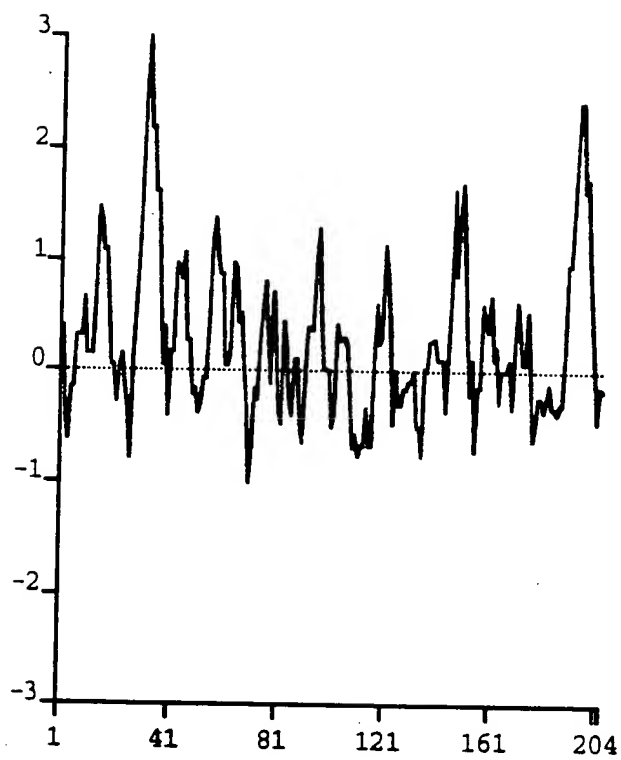


FIGURE 7

006260" 26529160

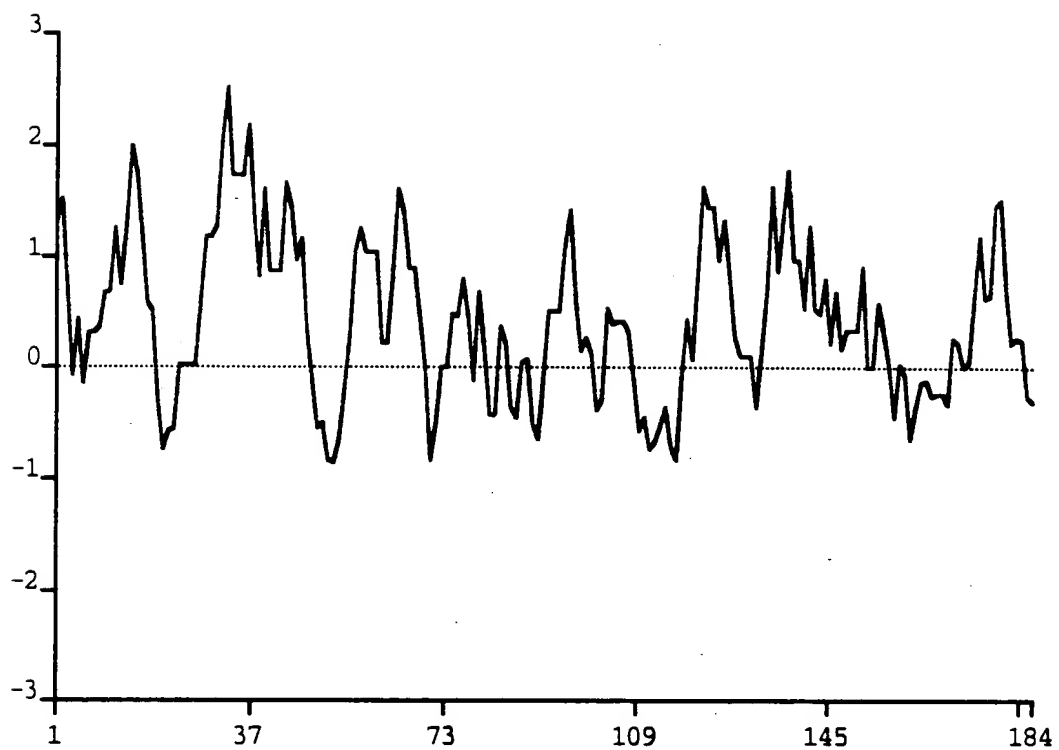


FIGURE 8

FIGURE 9

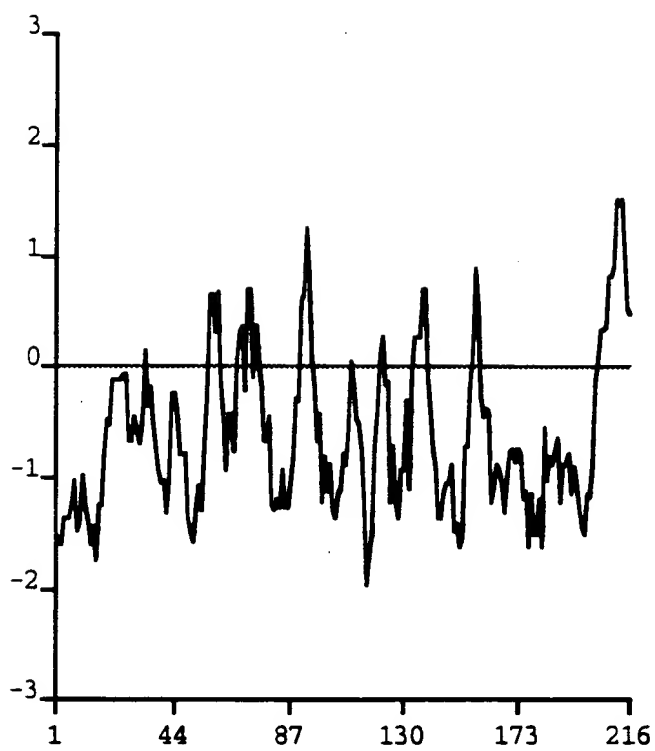


FIGURE 10

866260 26529T60

APPROVED	O.G. FIG. none	
BY	CLASS	SUBCLASS
DRAFTSMAN	530	350

6043343

9	18	27	36	45	54
5' GCC AGC TGC GTT CTG AGC CTG GGC GCA GCT ACC ATC TGC TCT GGG AAG CAC CAG					
63	72	81	90	99	108
GGT GTC CCC GCC CTC AGC TCG AAG TCA GCC ACC ATG GAG GCG CAG GCA CAA					
				M E A Q A Q	
117	126	135	144	153	162
GGT TTG TTG GAG ACT GAA CCG TTG CAA GGA ACA GAC GAA GAT GCA GTA GCC AGT					
G L L E T E P L Q G T D E D A V A S					
171	180	189	198	207	216
GCT GAC TTC TCT AGC ATG CTC TCT GAG GAG GAA AAG GAA GAG TTA AAA GCA GAG					
A D F S S M L S E E E K E E L K A E					
225	234	243	252	261	270
TTA GTT CAG CTA GAA GAC GAA ATT ACA ACA CTA CGA CAA GTT TTG TCA GCG AAA					
L V Q L E D E I T T L R Q V L S A K					
279	288	297	306	315	324
GAA AGG CAT CTA GTT GAG ATA AAA CAA AAA CTC GGC ATG AAC CTG ATG AAT GAA					
E R H L V E I K Q K L G M N L M N E					
333	342	351	360	369	378
TTA AAA CAG AAC TTC AGC AAA AGC TGG CAT GAC ATG CAG ACT ACC ACT GCC TAC					
L K Q N F S K S W H D M Q T T T A Y					

FIGURE 1A

15

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

387	396	405	414	423	432
AAG AAA ACA CAT GAA ACC CTG AGT CAC GCA GGG CAA AAG GCA ACT GCA GCT TTC					
K K T H E T L S H A G Q K A T A A F					
441	450	459	468	477	486
AGC AAC GTT GGA ACG GCC ATC AGC AAG AAG TTC GGA GAC ATG AGT TAC TCC ATT					
S N V G T A I S K K F G D M S Y S I					
495	504	513	522	531	540
CGC CAT TCC ATA AGT ATG CCT GCT ATG AGG AAT TCT CCT ACT TTC AAA TCA TTT					
R H S I S M P A M R N S P T F K S F					
549	558	567	576	585	594
GAG GAG AGG GTT GAG ACA ACT GTC ACA AGC CTC AAG ACG ACG AAA GTA GGC GGT ACG					
E E R V E T T V T S L K T K V G G T					
603	612	621	630	639	648
AAC CCT AAT GGA GGC AGT TTT GAG GAG GTC CTC AGC TCC ACG GCC CAT GCC AGT					
N P N G G S F E E V L S S T A H A S					
657	666	675	684	693	702
GCC CAG AGC TTG GCA GGA GGC TCC CGG CGG ACC AAG GAG GAG GAG CTG CAG TGC					
A Q S L A G G S R R T K E E L Q C					
711	720	729	738	747	756
TAA GTC CAG CCA GCG TGC AGT GCA TCC AGA AAC CGG CCA CTA CCC AGC CCA TCT					

FIGURE 1B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

865250" 6529160

765
NTG CCT GTG CTT ATC CAG ATA AGA AGA CCA AA 3'

774

783

FIGURE 1C

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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          9      18      27      36      45      54
5' TMG MKC GCG GGC CCC CGC CAG TCA GGT GGG TGC CAG GCC CTG GCC GTG GCG AAA

          63      72      81      90      99      108
GAG CCG GCG GAG GGA GGA CCC GCT CCC GGA GAC GCC GCC TCG CGA TCC CCG CGC

          117      126      135      144      153      162
GGG CGG GAC CGG GCG GCC GGC ATC ATG ACC CTG TTT CAC TTC GGG AAC TGC TTC
          M T L F H F G N C F

          171      180      189      198      207      216
GCT CTT GCC TAC TTC CCC TAC TTC ATC ACC TAC AAG TGC AGC GGC CTG TCC GAG
A L A Y F P Y F I T Y K C S G L S E

          225      234      243      252      261      270
TAC AAC GCC TTC TGG AAA TGC GTC CAG GCT GGA GTC ACC TAC CTC TTT GTC CAA
Y N A F W K C V Q A G V T Y L F V Q

          279      288      297      306      315      324
CTC TGC AAG ATG CTG TTC TTG GCC ACT TTC TTT CCC ACC TGG GAA GGC GGC ATC
L C K M L F L A T F F P T W E G G I

          333      342      351      360      369      378
TAT GAC TTC ATT GGG GAG TTC ATG AAG GCC AGC GTG GAT GTG GCA GAC CTG ATA
Y D F I G E F M K A S V V A D L I

```

FIGURE 2A

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

387	396	405	414	423	432
GGT CTA AAC CTT GTC ATG TCC CGG AAT GCC GGC AAG GGA GAG TAC AAG ATC ATG					
G L N L V M S R N A G K G E Y K I M					
441	450	459	468	477	486
GTT GCT GCC CTG GGC TGG GCC ACT GCT GAG CTT ATT ATG TCC CGC TGC ATT CCC					
V A A L G W A T A E L I M S R C I P					
495	504	513	522	531	540
CTA TGG GTC GGA GCC CGG GGC ATT GAG TTT GAC TGG AAG TAC ATC CAG ATG AGC					
L W V G A R G I E F D W K Y I Q M S					
549	558	567	576	585	594
ATA GAC TCC AAC ATC AGT CTG GTC CAT TAC ATC GTC GCG TCT GCT CAG GTC TGG					
I D S N I S L V H Y I V A S A Q V W					
603	612	621	630	639	648
ATG ATA ACA CGC TAT GAT CTG TAC CAC AAC TTC CGG CCA GCT GTC CTT CTG CTG					
M I T R Y D L Y H N F R P A V L L L					
657	666	675	684	693	702
ATG TTC CTC AGT GTC TAC AAG GCC TTT GTT ATG GAG ACC TTC GTC CAC CTC TGC					
M F L S V Y K A F V M E T F V H L C					
711	720	729	738	747	756
TCG CTG GGC AGT TGG GCA RCT CTA MTG GCC CGA GCA GTG GTA ACG GGC CTG CTG					
S L G S W A X L X A R A V V T G L L					

FIGURE 2B

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

060260 26529T60

765	774	783	792	801	810
GCC CTC AAG CAC TTT GGS CCT GTA TGT CGS CGT TGT CAA TGT GCA CTY CTA GGC					
A L K H F G P V C R R C Q C A L L G					
819	828	837	846	855	864
TTG GTG TCT CAG ACA TTG ATG TAC CTT TTC CCT GCC TCA CTC CAG GTT TTA GTG					
L V S Q T L M Y L F P A S L Q V L V					
873	882				
AAG TAA ACA GTA TTT GGA AAG TT 3'					
K					

FIGURE 2C

866260 26529483

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

Library	Lib Description	Abun	Pct Abun
BRAINOM02	brain, 55 M, NORM, WM	1	0.0454
UTRSNOT01	uterus, 59 F	1	0.0393
TLYMNOR01	lymphocytes (non-adher PEMNC), 24 M, RP	1	0.0372
BRSTNOT02	breast, 55 F, match to BRSTTUT01	2	0.0317
PROSTUT08	prostate tumor, 60 M, match to PROSNOT14	1	0.0266
PROSNOT14	prostate, 60 M, match to PROSTUT08	1	0.0256
LIVRNOM01	liver, 49 M, WM	1	0.0254
PROSNOT15	prostate, 66 M, match to PROSTUT10	1	0.0241
NERVMSM01	multiple sclerosis, 46 M, NORM, WM	1	0.0228
HNT2AGT01	hNT2 cell line, post-mitotic neurons	1	0.0190
BRAITUT02	brain tumor, metastasis, 58 M	1	0.0169
LIVSFEM02	liver/spleen, fetal M, NORM, WM	2	0.0053

Electronic Northern Results returned a total of 12 row(s).

FIGURE 3

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

Library	Lib Description	Abun	Pct Abun
COLNNOT22	colon, 56 F	2	0.0554
COLNPOT01	colon polyp, 40 F	2	0.0513
PROSNOT18	prostate, hyperplasia, 58 M	2	0.0513
MUSCNOT02	muscle, psoas, 12 M	1	0.0382
STOMTUT01	stomach tumor, 52 M, match to STOMNOT02	1	0.0368
SINTNOT02	small intestine, 55 F	1	0.0337
LVENNOT03	heart, left ventricle, 31 M	1	0.0337
MMLR3DT01	macrophages (adher PBMC), M/F, 72-hr MLR	1	0.0331
PROSTUT01	prostate tumor, 50 M, match to PROSNOT02	1	0.0310
LUNGUT03	lung tumor, 69 M, match to LUNGNOT15	1	0.0308
BLADTUT02	bladder tumor, 80 F, match to BLADNOT03	1	0.0305
BRAITUT08	brain tumor, astrocytoma, 47 M	2	0.0293
PROSTUT12	prostate tumor, 65 M, match to PROSNOT20	1	0.0279
BLADNOT04	bladder, 28 M	1	0.0278
TESTTUT02	testicular tumor, 31 M	1	0.0278
THYRNOT03	thyroid tumor, adenoma, 28 F	2	0.0277
SINTNOT13	small intestine, ileum, ulcerative colitis, 25 F	1	0.0275
COLNTUT03	colon tumor, 62 M, match to COLNNOT16	1	0.0272
BLADTUT05	bladder tumor, 66 M, match to BLADNOT06	1	0.0268
KIDNTUT01	kidney tumor, Wilms, 8m F	1	0.0267
PENITUT01	penis tumor, carcinoma, 64 M	1	0.0267
COLNNOT23	colon, 16 M	1	0.0264
BRAITUT13	brain tumor, meningioma, 68 M	1	0.0262

FIGURE 4A

365260" 26529760

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

LIVRTUT01	liver tumor, metastasis, 51 F	1	0.0259
PROSNOT14	prostate, 60 M, match to PROSTUT08	1	0.0256
BRSTTUT08	breast tumor, 45 F, match to BRSTNOT09	1	0.0254
BMARNOT03	bone marrow, 16 M	1	0.0242
RATRNOT02	heart, right atrium, 39 M	1	0.0236
PANCNOT01	pancreas, 29 M	1	0.0214
LUNGNOT04	lung, 2 M	1	0.0183
SYNORAT04	synovium, wrist, rheumatoid, 62 F	1	0.0174
PLACNOT02	placenta, fetal F	1	0.0168
BRSTNOT03	breast, 54 F, match to BRSTTUT02	1	0.0147
SPLNNOT04	spleen, 2 M	1	0.0128
PROSNOT06	prostate, 57 M, match to PROSTUT04	1	0.0114
LUNGFET03	lung, fetal F	1	0.0091

Electronic Northern Results returned a total of 36 row(s).

FIGURE 4B

FIGURE 5

APPROVED	D.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

1 M T L F H F G N C F A L A Y F F P Y F I T Y K C S G L S E Y N A F W K C V Q A G V SEQ ID NO-3
1 M S F F H F I N C F A L A F A P Y F I V Y K Y S G I N E Y S S I W K C A T A S G SEQ ID NO-7

41 T Y L F V Q L C K M L F L A T F F P T W E G G I Y D F I G E F F M K A S V D V A D SEQ ID NO-3
41 G Y L L T Q L A K L L I I A T F F P A L D S E G F S I V P E F L K S S A D I I D SEQ ID NO-7

81 L I G L N L V M S R - N A G K G E Y K I M V A A L G W A T A E L I M S R C I P L SEQ ID NO-3
81 V I G L H L L M T N F L A C K G E V R F V V G G L G W G F A H S V A H R L V L L SEQ ID NO-7

120 W V G A R G I E F D W K Y I Q M S I D S N I S L V H Y I V A S A Q V W M I T R Y SEQ ID NO-3
121 W V G A R G T A F T W R W V Q T S L D S S A D L L V I V S L A C L T W M I T R - SEQ ID NO-7

160 D L Y H N F R P A V L L L M F L S V Y K A F V M E T F V H L C S L G S W A R L D SEQ ID NO-3
160 - - - - - T P N K F L V S - - P I L A I T V Q H T F - - - S L Y G W S L L A SEQ ID NO-7

200 A R - - - A V V T G L L A L K H F G P V C R C Q C A L L G L V S Q T L M Y L F SEQ ID NO-3
188 F R F A Y S I A T A I L T V V V Y S A - - N R T A S T R K N - - - - - SEQ ID NO-7

237 P A S L O V L V K SEQ ID NO-3
216 - - - - - E SEQ ID NO-7

FIGURE 6

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

866260" 46529T60 11 82

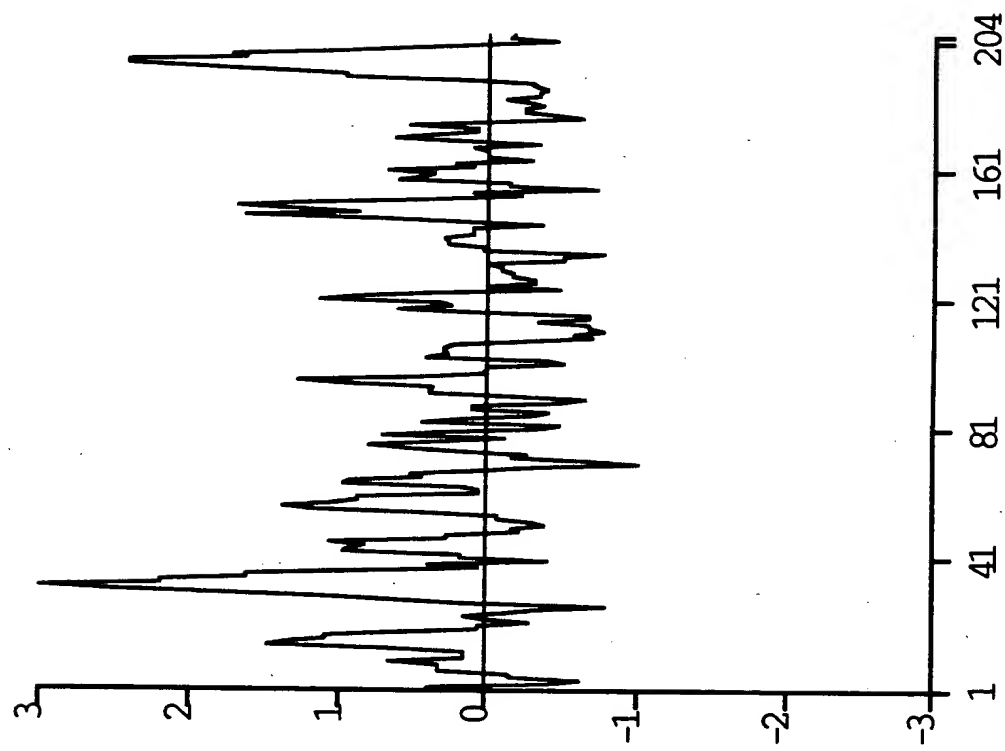


FIGURE 7

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

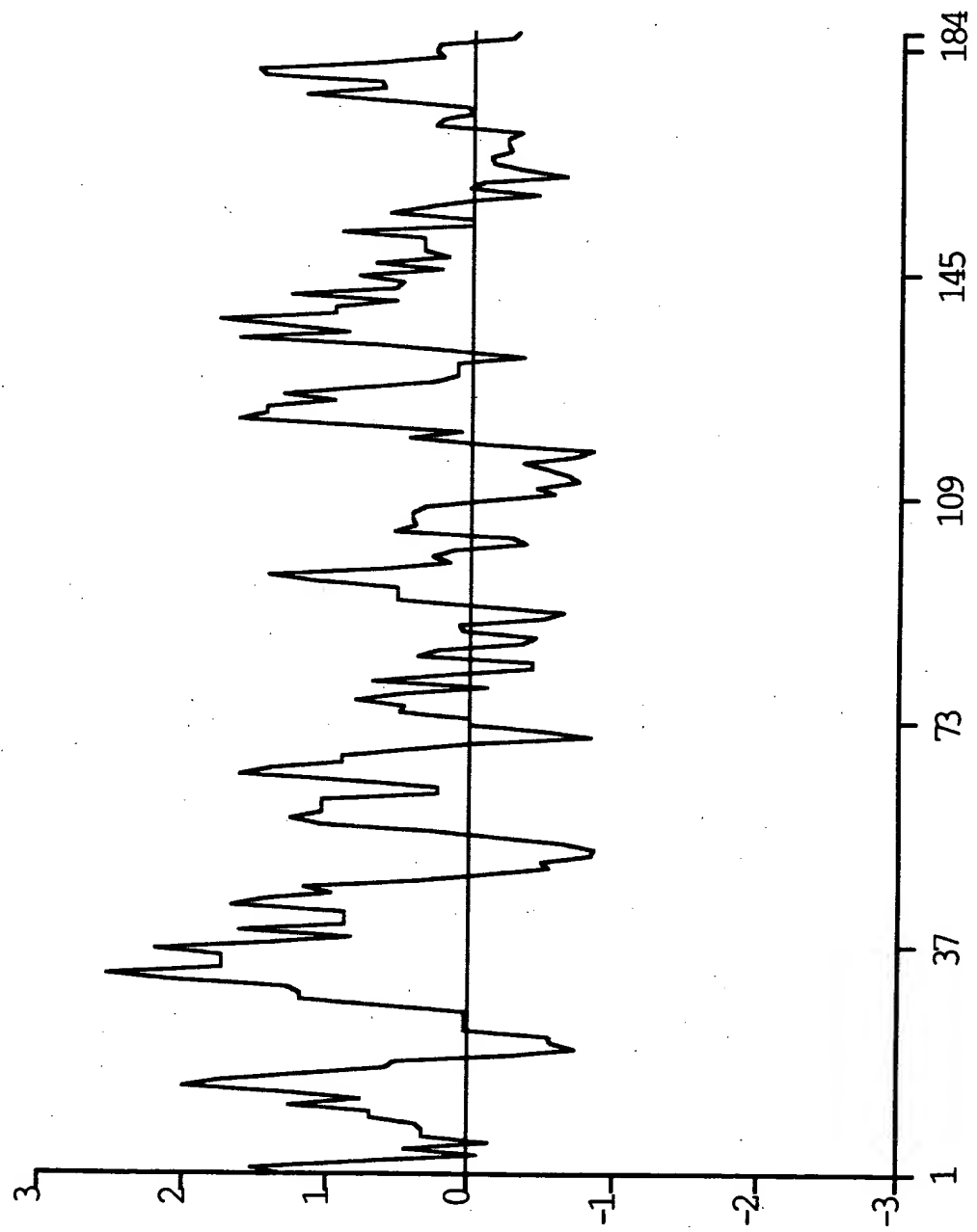


FIGURE 8

865250" 46529150

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

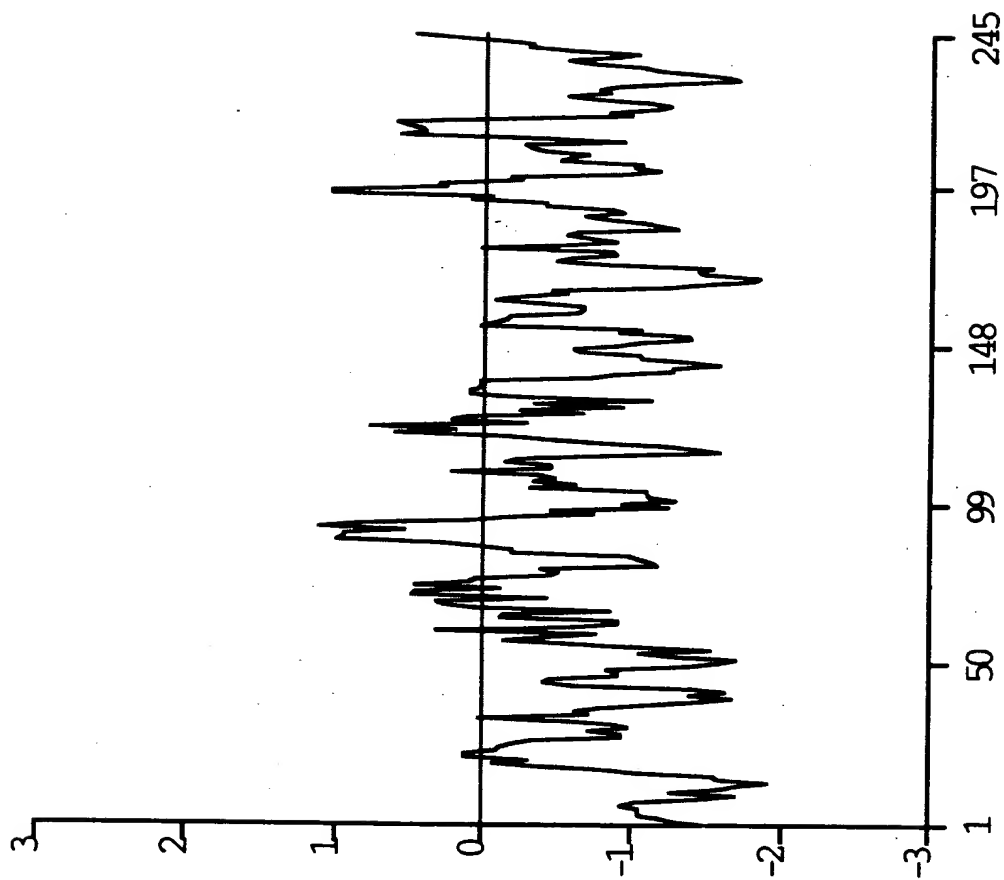


FIGURE 9

865260-4529153

APPROVED	O.G. FIG.	
BY-	CLASS	SUBCLASS
CRAFTSMAN		

865260" 26529760

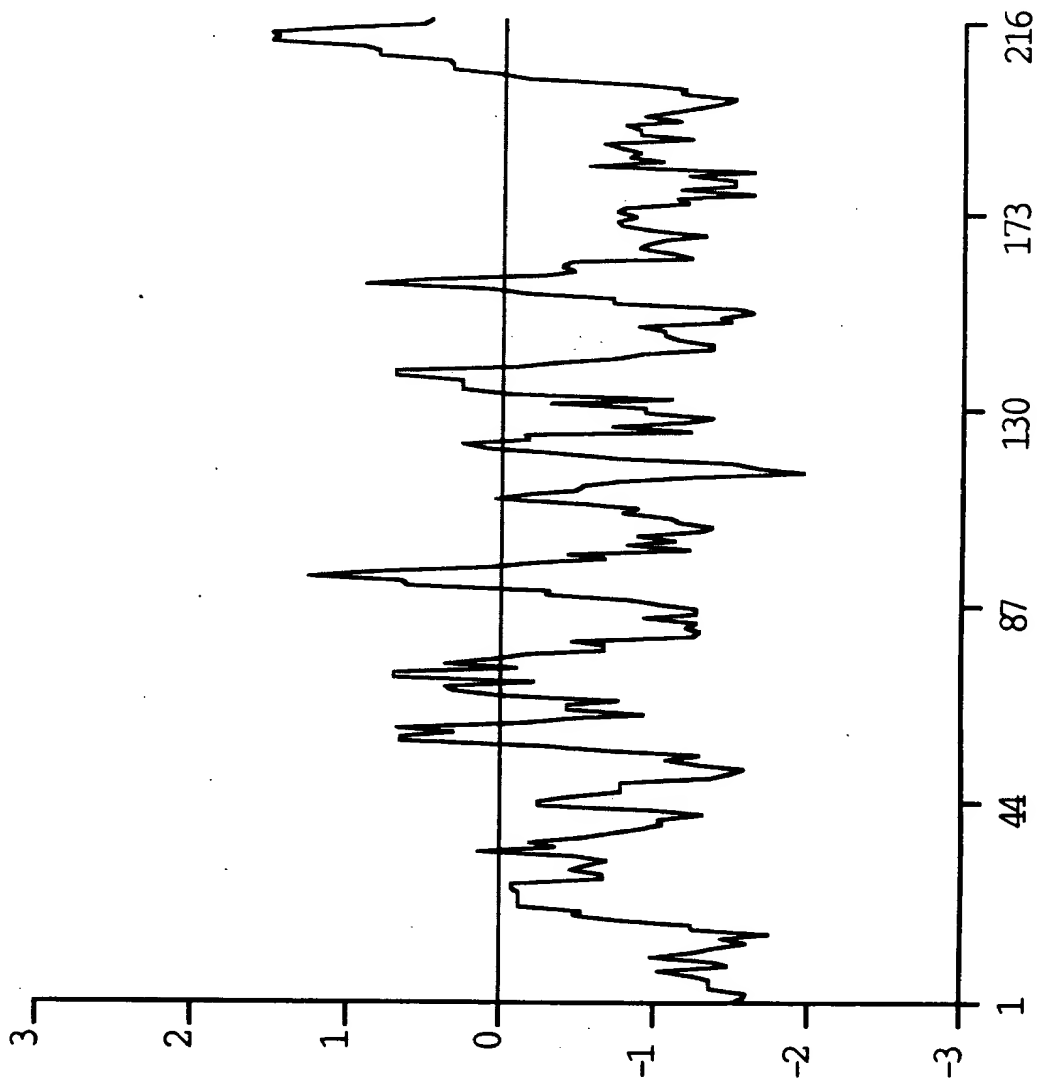


FIGURE 10